

# Supplementary Materials

Algae 2022, 37(3): 205-211

<https://doi.org/10.4490/algae.2022.37.9.11>

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## Concatenated (*rbcl* and *nrSSU*) data set: Outgroups from Yang et al. (2020)

125 taxa with 4 partitions and 3304 total sites

Partition	No. of Sites	Unique sites	Informative sites	Invariant sites
<i>rbcl</i> codon1	489	149	48	416
<i>rbcl</i> codon2	489	102	5	466
<i>rbcl</i> codon3	489	456	379	68
SSU	1837	741	385	1251

Best-fit model according to BIC:

<i>rbcl</i> codon1	GTR+F+I+G4
<i>rbcl</i> codon2	F81+F+I
<i>rbcl</i> codon3	TVM+F+I+G4
SSU	GTR+F+I+G4

Maximum Log-likelihood of the tree: -30218.4689

## Concatenated (*rbcl* and *nrSSU*) data set: Outgroups “Bangia 3” from Sutherland et al. (2011)

121 taxa with 4 partitions and 3322 total sites

Partition	No. of Sites	Unique sites	Informative sites	Invariant sites
<i>rbcl</i> codon1	489	143	44	423
<i>rbcl</i> codon2	489	98	3	472
<i>rbcl</i> codon3	489	441	356	85
SSU	1855	605	305	1406

Best-fit model according to BIC:

<i>rbcl</i> codon1	TIM+F+I+G4
<i>rbcl</i> codon2	F81+F+I
<i>rbcl</i> codon3	GTR+F+I+G4
SSU	SYM+I+G4

Maximum Log-likelihood of the tree: -25625.0053

### MrBayes 3.2 commands

#### Partition

```
charset rbclcodon1 = 1-xxxx\3;  
charset rbclcodon2 = 2-xxxx\3;  
charset rbclcodon3 = 3-xxxx\3;  
charset SSU = xxxx-xxxx;  
partition allpart = 4: rbclcodon1, rbclcodon2, rbclcodon3, SSU; set partition = allpart;  
lset applyto=(all) nst=6 rates=invgamma ngammat=4; prset applyto=(all) ratepr=variable;  
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);  
mcmc ngen=3000000 nruns=2 nchains=4 samplefreq=1000 printfreq=1000  
savebrlens=yes;  
sumt nruns=2 contype=allcompat filename=3gene burnin=300;
```

**Supplementary Fig S1.** Output data from the two dataset analysis, including variation in partitions, models selected per partition and -Log likelihood scores of maximum-likelihood tree, for the two different analyses. Bayesian parameters for MrBayes analysis are also shown.